SEQUENCE LISTING

<110> Lim, Moon Young
     Edwards, Cynthia A.
     Fry, Kirk E.
     Bruice, Thomas W.
     Starr, Douglas B.
     Laurance, Megan E.
     Kwok, Yan

<120> DNA Binding Compound-Mediated Molecular
  Switch System

<130> 54600-8130.US00

<140> US 09/518,297
<141> 2000-03-03

<150> US 60/122,513
<151> 1999-03-03

<150> US 60/154,605
<151> 1999-09-17

<160> 77

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<400> 1
cgttcgcact t   11

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cggagtactg tcctccg   17

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<223> n = A,T,C or G

<400> 3
taattanggg ng   12

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<211> 551
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<213> Homo sapiens

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<223> transcriptional regulatory protein

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Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
                20                  25                  30
Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
            35                  40                  45
Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
    50                  55                  60
Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
65                  70                  75                  80
Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
                85                  90                  95
Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
            100                 105                 110
Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
        115                 120                 125
Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
    130                 135                 140
Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
145                 150                 155                 160
Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
                165                 170                 175
Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
            180                 185                 190
Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
        195                 200                 205
Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
    210                 215                 220
Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
225                 230                 235                 240
Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
            245                 250                 255
Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu
        260                 265                 270
Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr
        275                 280                 285
Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg
    290                 295                 300
Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly
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305                     310                     315                     320
Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg
                325                     330                     335
Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr
                340                     345                     350
Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe
                355                     360                     365
Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro
        370                     375                     380
Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val
385                     390                     395                     400
Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly
                405                     410                     415
Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly
                420                     425                     430
Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu
                435                     440                     445
Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr
        450                     455                     460
Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln
465                     470                     475                     480
Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr
                485                     490                     495
Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp
                500                     505                     510
Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
        515                     520                     525
Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala
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Leu Leu Ser Gln Ile Ser Ser
545                     550

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<212> DNA
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<400> 5
tccctatcag tgatagaga                                                    19

<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> response element

<400> 6
cttaacactc gcgagtgtta ag                                                22

<210> 7
<211> 13
<212> DNA
<213> Artificial Sequence
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<223> n = A,T,C or G

<221> misc_feature
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rgntcantga cny   13

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<400> 8
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<210> 9

<400> 9
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 10

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 1               5                  10              15
Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
            20                  25              30
Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
        35                  40                  45
Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
    50                  55                  60
Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
65                  70                  75                  80
Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
                85                  90                  95
Val
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<210> 11
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> repressor sequence

4

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<400> 11
Met Ala Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala
 1               5                  10                  15
Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser
            20                  25                  30
Met Leu Pro Tyr
        35


<210> 12
<211> 116
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (0)...(0)
<223> partial promoter sequence

<400> 12
cgcggtcaga aaattatttt aaatttcctc ttgtcaggcc ggaataactc cctataatgc      60
gccaccactg acacggaaca acggcaaaca cgccgccggg tcagcggggt tctcct         116


<210> 13
<211> 22
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (0)...(0)
<223> partial promoter sequence

<400> 13
agaaaattat tttaaatttc ct                                              22


<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence

<400> 14
gactgcagtg gtacctagga gg                                              22


<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence

<400> 15
agaaaattat tttaaatttc ct                                              22


<210> 16
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<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence

<400> 16
ggaaaatttt ttttcaaaag ta                                              22

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence

<400> 17
tgaaatttat tttgcgaaag gg                                              22

<210> 18
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 18
tgttcgcact t                                                          11

<210> 19
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 19
catggacgcc actgagccgt ttttgttcgc acttgaggcg agtcgatgca cc            52

<210> 20
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 20
catggacgcc actgagccgt gttcgcactt tttttgagg cgagtcgatg cacc           54

<210> 21
<211> 58
<212> DNA
<213> Artificial Sequence
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<220>
<223> engineered DNA response element

<400> 21
catggacgcc actgagccgt ttttgttcgc acttttttttt gaggcgagtc gatgcacc          58

<210> 22
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 22
cttaaaaata ac                                                              12

<210> 23
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 23
ttgaaaaatc aacgct                                                          16

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 24
tttttgttcg cactttttttt t                                                   21

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 25
tttttgggat tttccttttt                                                      20

<210> 26
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 26
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7

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aaaaaattgt gagcgctcac aattttttt                                        28

<210> 27
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> tissue-specific transcription factor

<400> 27
acttta                                                                  6

<210> 28
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 28
taccgacat                                                               9

<210> 29
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 29
gggactttcc                                                             10

<210> 30
<211> 10
<212> DNA

<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 30
gggattttcc                                                             10

<210> 31
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 31
cgaccgtgct cgagttaacg ggactttcca aaaacgatcg gactggactc                 50

<210> 32
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<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 32
cgaccgtgct cgagttaacg ggattttcca aaaacgatcg gactggactc                50

<210> 33
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 33
cgaccgtgct cgagaaattg ggattttcca aaaacgatcg gactggactc                50

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 34
aaaaaattgt gagcgctcac aattttttt                                       28

<210> 35
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 35
ttttttttgt gagcggataa caaaa                                           25

<210> 36
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 36
tctgggatcc                                                            10

<210> 37
<211> 14
<212> DNA
<213> Artificial Sequence
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<220>
<223> engineered DNA response element

<400> 37
gagttttttt taag   14

<210> 38
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 38
gagttttaaa agag   14

<210> 39
<211> 969
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (0)...(0)
<223> transcriptional regulatory protein

<400> 39

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Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val Phe Gln
             20                  25                  30
Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln Ile Leu
         35                  40                  45
Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly
     50                  55                  60
Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys
65                  70                  75                  80
Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val
                 85                  90                  95
Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His
                100                 105                 110
Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val Thr Ala
             115                 120                 125
Gly Pro Lys Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His
         130                 135                 140
Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu
145                 150                 155                 160
Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro Asp Leu
                165                 170                 175
Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly Asp Arg
             180                 185                 190
Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys Glu Met
             195                 200                 205
Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser
         210                 215                 220
Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile
225                 230                 235                 240
Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met
```

10

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                    245                    250                    255
Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu
            260                    265                    270
Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu
        275                    280                    285
Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
    290                    295                    300
Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
305                    310                    315                    320
Asp Ile Asn Ile Thr Lys Pro Ala Ser Val Phe Val Gln Leu Arg Arg
            325                    330                    335
Lys Ser Asp Leu Glu Thr Ser Glu Pro Lys Pro Phe Leu Tyr Tyr Pro
            340                    345                    350
Glu Ile Lys Asp Lys Glu Glu Val Gln Arg Lys Arg Gln Lys Leu Met
        355                    360                    365
Pro Asn Phe Ser Asp Ser Phe Gly Gly Gly Ser Gly Ala Gly Ala Gly
    370                    375                    380
Gly Gly Gly Met Phe Gly Ser Gly Gly Gly Gly Gly Gly Thr Gly Ser
385                    390                    395                    400
Thr Gly Pro Gly Tyr Ser Phe Pro His Tyr Gly Phe Pro Thr Tyr Gly
            405                    410                    415
Gly Ile Thr Phe His Pro Gly Thr Thr Lys Ser Asn Ala Gly Met Lys
            420                    425                    430
His Gly Thr Met Asp Thr Glu Ser Lys Lys Asp Pro Glu Gly Cys Asp
        435                    440                    445
Lys Ser Asp Asp Lys Asn Thr Val Asn Leu Phe Gly Lys Val Ile Glu
    450                    455                    460
Thr Thr Glu Gln Asp Gln Glu Pro Ser Glu Ala Thr Val Gly Asn Gly
465                    470                    475                    480
Glu Val Thr Leu Thr Tyr Ala Thr Gly Thr Lys Glu Glu Ser Ala Gly
            485                    490                    495
Val Gln Asp Asn Leu Phe Leu Glu Lys Ala Met Gln Leu Ala Lys Arg
        500                    505                    510
His Ala Asn Ala Leu Phe Asp Tyr Ala Val Thr Gly Asp Val Lys Met
        515                    520                    525
Leu Leu Ala Val Gln Arg His Leu Thr Ala Val Gln Asp Glu Asn Gly
    530                    535                    540
Asp Ser Val Leu His Leu Ala Ile Ile His Leu His Ser Gln Leu Val
545                    550                    555                    560
Arg Asp Leu Leu Glu Val Thr Ser Gly Leu Ile Ser Asp Asp Ile Ile
            565                    570                    575
Asn Met Arg Asn Asp Leu Tyr Gln Thr Pro Leu His Leu Ala Val Ile
        580                    585                    590
Thr Lys Gln Glu Asp Val Val Glu Asp Leu Leu Arg Ala Gly Ala Asp
        595                    600                    605
Leu Ser Leu Leu Asp Arg Leu Gly Asn Ser Val Leu His Leu Ala Ala
    610                    615                    620
Lys Glu Gly His Asp Lys Val Leu Ser Ile Leu Leu Lys His Lys Lys
625                    630                    635                    640
Ala Ala Leu Leu Leu Asp His Pro Asn Gly Asp Gly Leu Asn Ala Ile
            645                    650                    655
His Leu Ala Met Met Ser Asn Ser Leu Pro Cys Leu Leu Leu Leu Val
        660                    665                    670
Ala Ala Gly Ala Asp Val Asn Ala Gln Glu Gln Lys Ser Gly Arg Thr
        675                    680                    685
Ala Leu His Leu Ala Val Glu His Asp Asn Ile Ser Leu Ala Gly Cys
    690                    695                    700
Leu Leu Leu Glu Gly Asp Ala His Val Asp Ser Thr Thr Tyr Asp Gly
705                    710                    715                    720
```

11

```
Thr Thr Pro Leu His Ile Ala Ala Gly Arg Gly Ser Thr Arg Leu Ala
                725             730             735
Ala Leu Leu Lys Ala Ala Gly Ala Asp Pro Leu Val Glu Asn Phe Glu
            740             745             750
Pro Leu Tyr Asp Leu Asp Asp Ser Trp Glu Asn Ala Gly Glu Asp Glu
            755             760             765
Gly Val Val Pro Gly Thr Thr Pro Leu Asp Met Ala Thr Ser Trp Gln
    770             775             780
Val Phe Asp Ile Leu Asn Gly Lys Pro Tyr Glu Pro Glu Phe Thr Ser
785             790             795             800
Asp Asp Leu Leu Ala Gln Gly Asp Met Lys Gln Leu Ala Glu Asp Val
            805             810             815
Lys Leu Gln Leu Tyr Lys Leu Leu Glu Ile Pro Asp Pro Asp Lys Asn
            820             825             830
Trp Ala Thr Leu Ala Gln Lys Leu Gly Leu Gly Ile Leu Asn Asn Ala
            835             840             845
Phe Arg Leu Ser Pro Ala Pro Ser Lys Thr Leu Met Asp Asn Tyr Glu
    850             855             860
Val Ser Gly Gly Thr Val Arg Glu Leu Val Glu Ala Leu Arg Gln Met
865             870             875             880
Gly Tyr Thr Glu Ala Ile Glu Val Ile Gln Ala Ala Ser Ser Pro Val
            885             890             895
Lys Thr Thr Ser Gln Ala His Ser Leu Pro Leu Ser Pro Ala Ser Thr
            900             905             910
Arg Gln Gln Ile Asp Glu Leu Arg Asp Ser Asp Ser Val Cys Asp Thr
            915             920             925
Gly Val Glu Thr Ser Phe Arg Lys Leu Ser Phe Thr Glu Ser Leu Thr
    930             935             940
Ser Gly Ala Ser Leu Leu Thr Leu Asn Lys Met Pro His Asp Tyr Gly
945             950             955             960
Gln Glu Gly Pro Leu Glu Gly Lys Ile
                965


<210> 40
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 40
gctagccccg ccccgttgac gcaaatgggc ggtaggcgtg tacggtggga ggtttatata    60
agcagagctc gtttagtgaa ccgtcagatc agatct                               96


<210> 41
<211> 154
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 41
gctagcgccc aaattgggat tttccaaaaa gccgaaattg ggattttcca aaaaccgccg    60
atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg tttatataag   120
cagagctcgt ttagtgaacc gtcagatcag atct                                154


<210> 42
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12

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<211> 212
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 42
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tagcgcccaa attgggattt tccaaaaagc cgaaattggg attttccaaa aaccgccgat     120
cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt tatataagca     180
gagctcgttt agtgaaccgt cagatcagat ct                                   212

<210> 43
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 43
gctagccccg ccccgttgac gcaaatgggc ggtaggcgtg tacggtggga ggtctatata      60
agcagagctc gtttagtgaa ccgtcagatc agatct                                96

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<212> DNA
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<220>
<223> engineered regulatory sequence

<400> 44
gctagcgccc aggtcgggat tttccgagga gccgaggtcg ggattttccg aggaccgccg      60
atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg cctatataag     120
cagagctcgt ttagtgaacc gtcagatcag atct                                 154

<210> 45
<211> 154
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 45
gctagcgccc aggtcgggat tttccgagga gccgaggtcg ggattttccg aggaccgccg      60
atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg cctatataag     120
cagagctcgt ttagtgaacc gtcagatcag atct                                 154

<210> 46
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered promoter construct
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13

<400> 46

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ggtacctcaa tattggccat tagccatatt attcattggt tatatagcat aaattaatat          60
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atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat         180
tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa         240
tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt         300
tcccatagta acgcaaatag ggattttcca ttaacgtcaa tgggtggagt atttacggta         360
aactgcccac ttggcagtac atcaagtgta tcatatgcca agtccgcccc ctattgacgt         420
caatgacggt aaatggcccg cctggcatta tgcccagtac atgactttat gggatttttcc        480
tatttggcag tacatctacg tattagtcat cgctattacc atggtgatgc ggttttggca         540
gtacaccaat gggcgtggat agcggtttga ctcacgggga tttccaagtc tccaccccat         600
tgacgtcaat gggagtttgt tttggcacca aggtaaaagg gattttccaa aatgtcgtaa         660
caactgcgat cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt         720
tatataagca gagctcgttt agtgaaccgt cagatcaagc tt                            762
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<210> 47
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered promoter construct

<400> 47

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tggctattgg ccattgcata cgttgtatct atatcataat atgtacattt atattggctc         120
atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat         180
tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa         240
tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt         300
tcccatagta acgcaaatat tcccgggaaa ttaacgtcaa tgggtggagt atttacggta         360
aactgcccac ttggcagtac atcaagtgta tcatatgcca agtccgcccc ctattgacgt         420
caatgacggt aaatggcccg cctggcatta tgcccagtac atgactttat tctcgaggaa         480
tatttggcag tacatctacg tattagtcat cgctattacc atggtgatgc ggttttggca         540
gtacaccaat gggcgtggat agcggtttga ctcacgggga tttccaagtc tccaccccat         600
tgacgtcaat gggagtttgt tttggcacca aggtaaaatt acgcgtaaaa aatgtcgtaa         660
caactgcgat cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt         720
gctagccgca gagctcgttt agtgaaccgt cagatcaagc tt                            762
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<210> 48
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered promoter construct

<400> 48

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ggtacctcaa tattggccat tagccatatt attcattggt tatatagcat aaatcaatat          60
tggctattgg ccattgcata cgttgtatct atatcataat atgtacattt atattggctc         120
atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat         180
tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa         240
tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt         300
tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggagt atttacggta         360
aactgcccac ttggcagtac atcaagtgta tcatatgcca agtccgcccc ctattgacgt         420
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